

DT  
12-18-00

1646

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/346,470A

DATE: 11/28/2000

TIME: 14:58:25

Input Set : A:\53-99.app

Output Set: N:\CRF3\11282000\I346470A.raw

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ENTERED  
see p.5

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3 <110> APPLICANT: Hill, Ronald J.
4   Hannan, Garry N.
6 <120> TITLE OF INVENTION: Genetic Sequences Encoding Steroid and Juvenile Hormone
7   Receptor Polypeptides and Insecticidal Modalities
8   Therefor
10 <130> FILE REFERENCE: 53-99
12 <140> CURRENT APPLICATION NUMBER: 09/346,470A
13 <141> CURRENT FILING DATE: 1999-07-01
15 <150> PRIOR APPLICATION NUMBER: WO 99/00033
16 <151> PRIOR FILING DATE: 1999-01-15
18 <150> PRIOR APPLICATION NUMBER: AU PP1356/98
19 <151> PRIOR FILING DATE: 1998-01-15
21 <160> NUMBER OF SEQ ID NOS: 20
23 <170> SOFTWARE: PatentIn Ver. 2.0
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 2274
27 <212> TYPE: DNA
28 <213> ORGANISM: Lucilia cuprina
30 <220> FEATURE:
31 <221> NAME/KEY: CDS
32 <222> LOCATION: (1)..(2271)
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36 Met Met Lys Arg Arg Trp Ser Asn Asn Gly Gly Phe Ala Ala Leu Lys
37   1           5           10           15
39 atg tta gaa gaa tcc tcc tca gaa gta acc tcc tcc tca aat ggt ctg   96
40 Met Leu Glu Glu Ser Ser Ser Glu Val Thr Ser Ser Ser Asn Gly Leu
41   20           25           30
43 gtc ttg tca tgg gat ata aat atg tca cct tcc tgg ttg gat tca ccc   144
44 Val Leu Ser Ser Asp Ile Asn Met Ser Pro Ser Ser Leu Asp Ser Pro
45   35           40           45
47 gtt tat ggc gat cag gaa atg tgg ctg tgt aac gat tca gct tca tat   192
48 Val Tyr Gly Asp Gln Glu Met Trp Leu Cys Asn Asp Ser Ala Ser Tyr
49   50           55           60
51 aat aac agt cat cag cat agt gtt ata act tgg ctg cag ggc tgc acc   240
52 Asn Asn Ser His Gln His Ser Val Ile Thr Ser Leu Gln Gly Cys Thr
53 65           70           75           80
55 tca tca ttg ccg gcc caa aca acc att ata cct ctg tca gct tta ccc   288
56 Ser Ser Leu Pro Ala Gln Thr Thr Ile Ile Pro Leu Ser Ala Leu Pro
57   85           90           95
59 aat tcc aat aat gcc tcc ctg aat aat caa aat caa aat tat caa aat   336
60 Asn Ser Asn Asn Ala Ser Leu Asn Asn Gln Asn Gln Asn Tyr Gln Asn
61   100          105          110
63 ggt aat tcc atg aat aca aat tta tgg gtt aac aca aat aac agt gtt   384
64 Gly Asn Ser Met Asn Thr Asn Leu Ser Val Asn Thr Asn Asn Ser Val
65   115          120          125
67 gga gga ggt gga ggt ggt ggt gta ccc ggt atg act tca ctc aat   432

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68 Gly Gly Gly Gly Gly Gly Gly Gly Val Pro Gly Met Thr Ser Leu Asn
69      130      135      140
71 ggt ctg ggt ggt ggt ggt ggc agt caa gtg aat aat cac aat cac agc 480
72 Gly Leu Gly Gly Gly Gly Gly Ser Gln Val Asn Asn His Asn His Ser
73 145      150      155      160
75 cac aat cat tta cac cac aac agc aac agt aat cac agt aat agc agt 528
76 His Asn His Leu His His Asn Ser Asn Ser Asn His Ser Asn Ser Ser
77      165      170      175
79 tcc cac cac aca aat ggc cac atg ggt att ggc ggc ggt ggt ggt ggc 576
80 Ser His His Thr Asn Gly His Met Gly Ile Gly Gly Gly Gly Gly Gly
81      180      185      190
83 tta tcg gtc aat att aat ggt ccc aat atc gtt agc aat gcc caa cag 624
84 Leu Ser Val Asn Ile Asn Gly Pro Asn Ile Val Ser Asn Ala Gln Gln
85      195      200      205
87 tta aac tcg tta cag gcc tca caa aat ggc caa gtt att cat gcc aat 672
88 Leu Asn Ser Leu Gln Ala Ser Gln Asn Gly Gln Val Ile His Ala Asn
89      210      215      220
91 att ggc att cac agt atc agt aat gga tta aat cat cat cac cat 720
92 Ile Gly Ile His Ser Ile Ile Ser Asn Gly Leu Asn His His His His
93 225      230      235      240
95 cat cat atg aat aac agt agt atg atg cat cat aca ccc aga tct gaa 768
96 His His Met Asn Asn Ser Ser Met Met His His Thr Pro Arg Ser Glu
97      245      250      255
99 tca gct aat tcc ata tca tca ggt cgt gat gat ctt tca ccc tcg agc 816
100 Ser Ala Asn Ser Ile Ser Ser Gly Arg Asp Asp Leu Ser Pro Ser Ser
101      260      265      270
103 agt ctt aat ggc ttc tca aca agc gat gct agt gat gtt aag aaa atc 864
104 Ser Leu Asn Gly Phe Ser Thr Ser Asp Ala Ser Asp Val Lys Lys Ile
105      275      280      285
107 aaa aaa ggt cct gcg ccc cgt tta caa gag gaa ctg tgt ctg gtg tgt 912
108 Lys Lys Gly Pro Ala Pro Arg Leu Gln Glu Glu Leu Cys Leu Val Cys
109      290      295      300
111 ggt gat cgg gcg tcc ggt tat cat tat aac gca ctc acc tgt gaa ggc 960
112 Gly Asp Arg Ala Ser Gly Tyr His Tyr Asn Ala Leu Thr Cys Glu Gly
113 305      310      315      320
115 tgt aag ggg ttc ttt cga cgg agt gtt acc aaa aat gcg gtg tat tgt 1008
116 Cys Lys Gly Phe Phe Arg Arg Ser Val Thr Lys Asn Ala Val Tyr Cys
117      325      330      335
119 tgt aaa ttt ggt cat gcc tgc gaa atg gac atg tat atg cga cgt aaa 1056
120 Cys Lys Phe Gly His Ala Cys Glu Met Asp Met Tyr Met Arg Arg Lys
121      340      345      350
123 tgt cag gaa tgt agg ctg aaa aaa tgt ttg gct gtg ggc atg cgg ccg 1104
124 Cys Gln Glu Cys Arg Leu Lys Lys Cys Leu Ala Val Gly Met Arg Pro
125      355      360      365
127 gaa tgt gtg gtg ccc gaa aac cag tgt gca atg aaa cga cgc gaa aag 1152
128 Glu Cys Val Val Pro Glu Asn Gln Cys Ala Met Lys Arg Arg Glu Lys
129      370      375      380
131 aaa gca caa aaa gag aag gat aaa ata cag acc agt gtg tgt gca acg 1200
132 Lys Ala Gln Lys Glu Lys Asp Lys Ile Gln Thr Ser Val Cys Ala Thr

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133	385	390	395	400	
135	gaa att aaa aag gaa ata ctc gat tta atg aca tgt gaa ccg cca tca				1248
136	Glu Ile Lys Lys Glu Ile Leu Asp Leu Met Thr Cys Glu Pro Pro Ser				
137		405	410	415	
139	cat cca acg tgt ccg ctg tta cct gaa gac att ttg gct aaa tgt caa				1296
140	His Pro Thr Cys Pro Leu Leu Pro Glu Asp Ile Leu Ala Lys Cys Glu				
141		420	425	430	
143	gct cgt aat ata cct cct tta tcg tac aat caa ttg gca gtt ata tat				1344
144	Ala Arg Asn Ile Pro Pro Leu Ser Tyr Asn Gln Leu Ala Val Ile Tyr				
145		435	440	445	
147	aaa tta ata tgg tat caa gat ggc tac gaa cag cca tcc gag gaa gat				1392
148	Lys Leu Ile Trp Tyr Gln Asp Gly Tyr Glu Gln Pro Ser Glu Glu Asp				
149		450	455	460	
151	ctc aaa cgt ata atg agt tca ccc gat gaa aat gaa agt caa cac gat				1440
152	Leu Lys Arg Ile Met Ser Ser Pro Asp Glu Asn Glu Ser Gln His Asp				
153		465	470	475	480
155	gca tca ttt cgt cat ata aca gaa atc act ata cta aca gta caa tta				1488
156	Ala Ser Phe Arg His Ile Thr Glu Ile Thr Ile Leu Thr Val Gln Leu				
157		485	490	495	
159	att gtg gaa ttg gcc aag ggt ttg cca gcg ttt acc aaa ata cca caa				1536
160	Ile Val Glu Phe Ala Lys Gly Leu Pro Ala Phe Thr Lys Ile Pro Gln				
161		500	505	510	
163	gag gat caa ata aca cta tta aag gcc tgc tca tca gaa gtt atg atg				1584
164	Glu Asp Gln Ile Thr Leu Leu Lys Ala Cys Ser Ser Glu Val Met Met				
165		515	520	525	
167	ttg cga atg gca cga cgt tac gat cac aat tca gat tcg ata ttc ttt				1632
168	Leu Arg Met Ala Arg Arg Tyr Asp His Asn Ser Asp Ser Ile Phe Phe				
169		530	535	540	
171	gcc aat aat cga tcg tat acg cgt gac tct tat aaa atg gct gcc atg				1680
172	Ala Asn Asn Arg Ser Tyr Thr Arg Asp Ser Tyr Lys Met Ala Gly Met				
173		545	550	555	560
175	gct gat aat att gag gat ctg ctg cat ttc tgt cga caa atg tac tcg				1728
176	Ala Asp Asn Ile Glu Asp Leu Leu His Phe Cys Arg Gln Met Tyr Ser				
177		565	570	575	
179	atg aaa gtg gac aat gtc gaa tat gct cta ctc act gcc att gtg atc				1776
180	Met Lys Val Asp Asn Val Glu Tyr Ala Leu Leu Thr Ala Ile Val Ile				
181		580	585	590	
183	ttt tcc gat cgg ccg ggt ctc gaa gaa gcc gaa cta gtc gaa gcg ata				1824
184	Phe Ser Asp Arg Pro Gly Leu Glu Glu Ala Glu Leu Val Glu Ala Ile				
185		595	600	605	
187	caa agt tac tac atc gat aca ctc cgc att tac ata ctt aat cgc cat				1872
188	Glu Ser Tyr Tyr Ile Asp Thr Leu Arg Ile Tyr Ile Leu Asn Arg His				
189		610	615	620	
191	tcg gcc gat ccc atg agt ctc gta ttc ttt gcc aag ctt ctg tca att				1920
192	Cys Gly Asp Pro Met Ser Leu Val Phe Phe Ala Lys Leu Leu Ser Ile				
193		625	630	635	640
195	cta acc gaa ctg cgt acg ttg ggc aat caa aat gcc gaa atg tgt ttc				1968
196	Leu Thr Glu Leu Arg Thr Leu Gly Asn Gln Asn Ala Glu Met Cys Phe				
197		645	650	655	

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199 tcg ttg aaa ttg aaa aat cgc aaa ctg cca aaa ttc ctc gaa gag atc 2016
200 Ser Leu Lys Leu Lys Asn Arg Lys Leu Pro Lys Phe Leu Glu Glu Ile
201          660          665          670
203 tgg gat gta cat gcc att cca ccc tca gtg cag tca cac ata cag gct 2064
204 Trp Asp Val His Ala Ile Pro Pro Ser Val Gln Ser His Ile Gln Ala
205          675          680          685
207 acc cag qcg gaa aag gcc gcc cag gaa qct cag qca aca aca tcg gcc 2112
208 Thr Gln Ala Glu Lys Ala Ala Gln Glu Ala Gln Ala Thr Thr Ser Ala
209          690          695          700
211 att tca gca gcc gcc acc tca tct tcc tcc ata aat acc tcg atg gca 2160
212 Ile Ser Ala Ala Ala Thr Ser Ser Ser Ile Asn Thr Ser Met Ala
213 705          710          715          720
215 aca tca tcc tca tca tcg tta tcg cca tcg qcg gcc tca aca ccc aat 2208
216 Thr Ser Ser Ser Ser Ser Leu Ser Pro Ser Ala Ala Ser Thr Pro Asn
217          725          730          735
219 qgt ggt gcc gtc gat tat gtt qgc acc gat atg agt atg agt tta gta 2256
220 Gly Gly Ala Val Asp Tyr Val Gly Thr Asp Met Ser Met Ser Leu Val
221          740          745          750
223 caa tcg gat aat gca tag 2274
224 Gln Ser Asp Asn Ala
225          755
228 <210> SEQ ID NO: 2
229 <211> LENGTH: 757
230 <212> TYPE: PRT
231 <213> ORGANISM: Lucilia cuprina
233 <400> SEQUENCE: 2
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235 1 5 10 15
237 Met Leu Glu Glu Ser Ser Ser Glu Val Thr Ser Ser Ser Asn Gly Leu
238 20 25 30
240 Val Leu Ser Ser Asp Ile Asn Met Ser Pro Ser Ser Leu Asp Ser Pro
241 35 40 45
243 Val Tyr Gly Asp Gln Glu Met Trp Leu Cys Asn Asp Ser Ala Ser Tyr
244 50 55 60
246 Asn Asn Ser His Gln His Ser Val Ile Thr Ser Leu Gln Gly Cys Thr
247 65 70 75 80
249 Ser Ser Leu Pro Ala Gln Thr Thr Ile Ile Pro Leu Ser Ala Leu Pro
250 85 90 95
252 Asn Ser Asn Asn Ala Ser Leu Asn Asn Gln Asn Gln Asn Tyr Gln Asn
253 100 105 110
255 Gly Asn Ser Met Asn Thr Asn Leu Ser Val Asn Thr Asn Asn Ser Val
256 115 120 125
258 Gly Gly Gly Gly Gly Gly Gly Val Pro Gly Met Thr Ser Leu Asn
259 130 135 140
261 Gly Leu Gly Gly Gly Gly Gly Ser Gln Val Asn Asn His Asn His Ser
262 145 150 155 160
264 His Asn His Leu His His Asn Ser Asn Ser Asn His Ser Asn Ser Ser
265 165 170 175
267 Ser His His Thr Asn Gly His Met Gly Ile Gly Gly Gly Gly Gly Gly

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Input Set : A:\53-99.app

Output Set: N:\CRF3\11282000\I346470A.raw

```

268      180      185      190
270 Leu Ser Val Asn Ile Asn Gly Pro Asn Ile Val Ser Asn Ala Gln Gln
271      195      200      205
273 Leu Asn Ser Leu Gln Ala Ser Gln Asn Gly Gln Val Ile His Ala Asn
274      210      215      220
276 Ile Gly Ile His Ser Ile Ile Ser Asn Gly Leu Asn His His His His
277 225      230      235      240
279 His His Met Asn Asn Ser Ser Met Met His His Thr Pro Arg Ser Glu
280      245      250      255
282 Ser Ala Asn Ser Ile Ser Ser Gly Arg Asp Asp Leu Ser Pro Ser Ser
283      260      265      270
285 Ser Leu Asn Gly Phe Ser Thr Ser Asp Ala Ser Asp Val Lys Lys Ile
286      275      280      285
288 Lys Lys Gly Pro Ala Pro Arg Leu Gln Glu Glu Leu Cys Leu Val Cys
289      290      295      300
291 Gly Asp Arg Ala Ser Gly Tyr His Tyr Asn Ala Leu Thr Cys Glu Gly
292 305      310      315      320
294 Cys Lys Gly Phe Phe Arg Arg Ser Val Thr Lys Asn Ala Val Tyr Cys
295      325      330      335
297 Cys Lys Phe Gly His Ala Cys Glu Met Asp Met Tyr Met Arg Arg Lys
298      340      345      350
300 Cys Gln Glu Cys Arg Leu Lys Lys Cys Leu Ala Val Gly Met Arg Pro
301      355      360      365
303 Glu Cys Val Val Pro Glu Asn Gln Cys Ala Met Lys Arg Arg Glu Lys
304      370      375      380
306 Lys Ala Gln Lys Glu Lys Asp Lys Ile Gln Thr Ser Val Cys Ala Thr
307 385      390      395      400
309 Glu Ile Lys Lys Glu Ile Leu Asp Leu Met Thr Cys Glu Pro Pro Ser
310      405      410      415
312 His Pro Thr Cys Pro Leu Leu Pro Glu Asp Ile Leu Ala Lys Cys Gln
313      420      425      430
315 Ala Arg Asn Ile Pro Pro Leu Ser Tyr Asn Gln Leu Ala Val Ile Tyr
316      435      440      445
318 Lys Leu Ile Trp Tyr Gln Asp Gly Tyr Glu Gln Pro Ser Glu Glu Asp
319      450      455      460
321 Leu Lys Arg Ile Met Ser Ser Pro Asp Glu Asn Glu Ser Gln His Asp
322 465      470      475      480
324 Ala Ser Phe Arg His Ile Thr Glu Ile Thr Ile Leu Thr Val Gln Leu
325      485      490      495
327 Ile Val Glu Phe Ala Lys Gly Leu Pro Ala Phe Thr Lys Ile Pro Gln
328      500      505      510
330 Glu Asp Gln Ile Thr Leu Leu Lys Ala Cys Ser Ser Glu Val Met Met
331      515      520      525
333 Leu Arg Met Ala Arg Arg Tyr Asp His Asn Ser Asp Ser Ile Phe Phe
334      530      535      540
336 Ala Asn Asn Arg Ser Tyr Thr Arg Asp Ser Tyr Lys Met Ala Gly Met
337 545      550      555      560
339 Ala Asp Asn Ile Glu Asp Leu Leu His Phe Cys Arg Gln Met Tyr Ser
340      565      570      575

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**Please Note:**

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

## VERIFICATION SUMMARY

PATENT APPLICATION: US/09/346,470A

DATE: 11/28/2000

TIME: 14:58:26

Input Set : A:\51-99.app

Output Set: N:\CRF3\11282000\I346470A.raw

L:1279 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15

L:1346 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20